

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number:

10/523,312A

Source:

IFW

Date Processed by STIC:

1/18/07

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 01/18/2007

PATENT APPLICATION: US/10/523,312A

TIME: 16:01:51

Input Set : A:\pto.kd.txt

Output Set: N:\CRF4\01182007\J523312A.raw

3 <110> APPLICANT: Berezenko, Stephen  
 4 Sadler, Peter J.  
 5 Stewart, Alan J.  
 6 Blindauer, Claudia  
 7 Bunyan, Kerry E.  
 9 <120> TITLE OF INVENTION: NOVEL ALBUMINS  
 11 <130> FILE REFERENCE: 63572-5001-US  
 13 <140> CURRENT APPLICATION NUMBER: US 10/523,312A  
 14 <141> CURRENT FILING DATE: 2005-01-26  
 16 <150> PRIOR APPLICATION NUMBER: GB217347.4  
 17 <151> PRIOR FILING DATE: 2002-07-26  
 19 <160> NUMBER OF SEQ ID NOS: 12  
 21 <170> SOFTWARE: PatentIn version 3.4  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 585  
 25 <212> TYPE: PRT  
 26 <213> ORGANISM: Artificial Sequence  
 28 <220> FEATURE:  
 29 <223> OTHER INFORMATION: Human heptocytes cell lines were treated with rHA or His67ALa  
 mutant  
 30 albumin to study their effects on the human heptocyte cell culture. The cell  
 31 line used was WRL-68.  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: misc\_feature  
 36 <222> LOCATION: (30)..(30)  
 37 <223> OTHER INFORMATION: X IS ANY AMINO ACID OTHER THAN Y  
 39 <220> FEATURE:  
 40 <221> NAME/KEY: misc\_feature  
 41 <222> LOCATION: (67)..(67)  
 42 <223> OTHER INFORMATION: X IS ANY AMINO ACID OTHER THAN H  
 44 <220> FEATURE:  
 45 <221> NAME/KEY: misc\_feature  
 46 <222> LOCATION: (99)..(100)  
 47 <223> OTHER INFORMATION: X IS ANY AMINO ACID OTHER THAN N  
 49 <220> FEATURE:  
 50 <221> NAME/KEY: misc\_feature  
 51 <222> LOCATION: (103)..(103)  
 52 <223> OTHER INFORMATION: X IS ANY AMINO ACID OTHER THAN E  
 54 <220> FEATURE:  
 55 <221> NAME/KEY: misc\_feature  
 56 <222> LOCATION: (146)..(146)  
 57 <223> OTHER INFORMATION: X IS ANY AMINO ACID OTHER THAN L  
 59 <220> FEATURE:  
 60 <221> NAME/KEY: misc\_feature

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Input Set : A:\pto.kd.txt

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61 <222> LOCATION: (242)..(242)  
 62 <223> OTHER INFORMATION: X IS ANY AMINO ACID OTHER THAN H  
 64 <220> FEATURE:  
 65 <221> NAME/KEY: misc\_feature  
 66 <222> LOCATION: (247)..(247)  
 67 <223> OTHER INFORMATION: X IS ANY AMINO ACID OTHER THAN H  
 69 <220> FEATURE:  
 70 <221> NAME/KEY: misc\_feature  
 71 <222> LOCATION: (248)..(248)  
 72 <223> OTHER INFORMATION: X IS ANY AMINO ACID OTHER THAN G  
 74 <220> FEATURE:  
 75 <221> NAME/KEY: misc\_feature  
 76 <222> LOCATION: (249)..(249)  
 77 <223> OTHER INFORMATION: X IS ANY AMINO ACID OTHER THAN D  
 79 <220> FEATURE:  
 80 <221> NAME/KEY: misc\_feature  
 81 <222> LOCATION: (288)..(288)  
 82 <223> OTHER INFORMATION: X IS ANY AMINO ACID OTHER THAN H  
 84 <400> SEQUENCE: 1  
 86 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu  
 87 1 5 10 15  
 W--> 90 Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Xaa Leu Gln  
 91 20 25 30  
 94 Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
 95 35 40 45  
 98 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
 99 50 55 60  
 102 Ser Leu Xaa Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
 103 65 70 75 80  
 106 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
 107 85 90 95  
 110 Glu Arg Xaa Xaa Cys Phe Xaa Gln His Lys Asp Asp Asn Pro Asn Leu  
 111 100 105 110  
 114 Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
 115 115 120 125  
 118 Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg  
 119 130 135 140  
 122 Arg Xaa Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg  
 123 145 150 155 160  
 126 Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala  
 127 165 170 175  
 130 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser  
 131 180 185 190  
 134 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu  
 135 195 200 205  
 138 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro  
 139 210 215 220  
 142 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys  
 143 225 230 235 240

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146 Val Xaa Thr Glu Cys Cys Xaa Xaa Xaa Leu Leu Glu Cys Ala Asp Asp
147          245          250          255
150 Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
151          260          265          270
154 Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser Xaa
155          275          280          285
158 Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
159          290          295          300
162 Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
163 305          310          315          320
166 Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
167          325          330          335
170 Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
171          340          345          350
174 Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
175          355          360          365
178 Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
179          370          375          380
182 Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
183 385          390          395          400
186 Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
187          405          410          415
190 Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
191          420          425          430
194 Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
195          435          440          445
198 Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
199          450          455          460
202 Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
203 465          470          475          480
206 Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
207          485          490          495
210 Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
211          500          505          510
214 Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
215          515          520          525
218 Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
219          530          535          540
222 Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
223 545          550          555          560
226 Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
227          565          570          575
230 Ala Ala Ser Gln Ala Ala Leu Gly Leu
231          580          585
234 <210> SEQ ID NO: 2
235 <211> LENGTH: 609
236 <212> TYPE: PRT
237 <213> ORGANISM: Artificial
239 <220> FEATURE:

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240 &lt;223&gt; OTHER INFORMATION: Human

242 &lt;400&gt; SEQUENCE: 2

```

244 Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
245 1 5 10 15
248 Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala
249 20 25 30
252 His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
253 35 40 45
256 Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
257 50 55 60
260 Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
261 65 70 75 80
264 Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
265 85 90 95
268 Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
269 100 105 110
272 Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
273 115 120 125
276 His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
277 130 135 140
280 Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
281 145 150 155 160
284 Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
285 165 170 175
288 Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
289 180 185 190
292 Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
293 195 200 205
296 Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys
297 210 215 220
300 Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
301 225 230 235 240
304 Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
305 245 250 255
308 Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
309 260 265 270
312 Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
313 275 280 285
316 Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
317 290 295 300
320 Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
321 305 310 315 320
324 Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
325 325 330 335
328 Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
329 340 345 350
332 Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
333 355 360 365
336 Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys

```

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```

337      370      375      380
340 Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
341 385      390      395      400
344 Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
345      405      410      415
348 Glu Leu Phe Glu Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
349      420      425      430
352 Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val
353      435      440      445
356 Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
357      450      455      460
360 Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
361 465      470      475      480
364 Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
365      485      490      495
368 Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
369      500      505      510
372 Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
373      515      520      525
376 Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
377      530      535      540
380 Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
381 545      550      555      560
384 Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
385      565      570      575
388 Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe
389      580      585      590
392 Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly
393      595      600      605
396 Leu
400 <210> SEQ ID NO: 3
401 <211> LENGTH: 600
402 <212> TYPE: PRT
403 <213> ORGANISM: Rhesus macaque
405 <400> SEQUENCE: 3
407 Leu Leu Phe Leu Phe Ser Ser Ala Tyr Ser Arg Gly Val Phe Arg Arg
408 1      5      10      15
411 Asp Thr His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
412      20      25      30
415 Glu His Phe Lys Gly Leu Val Leu Val Ala Phe Ser Gln Tyr Leu Gln
416      35      40      45
419 Gln Cys Pro Phe Glu Glu His Val Lys Leu Val Asn Glu Val Thr Glu
420      50      55      60
423 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
424 65      70      75      80
427 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
428      85      90      95
431 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
432      100      105      110

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/523,312A

DATE: 01/18/2007  
TIME: 16:01:52

Input Set : A:\pto.kd.txt  
Output Set: N:\CRF4\01182007\J523312A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 30,67,99,100,103,146,242,247,248,249,288

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:2

VERIFICATION SUMMARY

DATE: 01/18/2007

PATENT APPLICATION: US/10/523,312A

TIME: 16:01:52

Input Set : A:\pto.kd.txt

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L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16

M:341 Repeated in SeqNo=1